WHAT IS CLAIMED IS:

1. A method of screening a population of nucleic acids for a novel sequence, the method comprising:

(a) providing a population of nucleic acid sequences;

(b) partitioning said population into one or more subpopulations of nucleic acids;

(c) identifying a first nucleic acid sequence in the subpopulation of nucleic acid sequences; and

(d) comparing the first nucleic acid sequence to a reference nucleic acid sequence or sequences, wherein the absence of the first nucleic acid sequence in the reference nucleic acid or nucleic acid sequences indicates the first nucleic acid is a novel nucleic acid sequence.

2. The method of claim 1, wherein said DNA population is a cDNA population derived from a population of RNA molecules.

3. The method of claim 2, further comprising partitioning the RNA molecules.

4. The method of claim 2, wherein said cDNA population is derived from the 5' ends of the RNA molecules.

5. The method of claim 2, wherein said cDNA population is derived from the interior regions of the RNA molecules.

6. The method of claim 2, wherein said cDNA population is derived from the 3' ends of the DNA molecules.

7. The method of claim 2, wherein said partitioning step comprises hybridization of a probe nucleic acid sequence to the population of nucleic acids.

8. The method of claim 2, wherein said partitioning step comprises digesting the cDNA molecules with one or more restriction enzymes.

9. The method of claim 8, further comprising ligating adapter oligonucleotides to the termini of the digested cDNA molecules.

10. The method of claim 9, further comprising amplifying the ligation products.

11. The method of claim 8, further comprising separating the amplified products.

12. The method of claim 11, wherein said separating is by gel electrophoresis.

13. The method of claim 11, wherein the first nucleic acid sequence is identified by comparing the size of one or more digestion products produced by a member of the subpopulation of nucleic acids to the sizes of fragments generated by the same restriction enzyme or enzymes in said reference nucleic acid or nucleic acids.

14. The method of claim 11, further comprising

(a) recovering one or more size-separated digestion products;

(b) reamplifying the recovered products; and

(c) separating the reamplified products.

15. The method of claim 14, wherein said separating is by gel electrophoresis.

16. The method of claim 15, wherein the first nucleic acid sequence is identified by comparing the size of one or more digestion products produced by a member of the subpopulation of nucleic acids to the sizes of fragments generated by the same restriction enzyme or enzymes in said reference nucleic acid or nucleic acids.

17. The method of claim 9, further comprising:

(a) inserting the ligated adapter oligonucleotide into a cloning vector to form a vector-insert;

(b) transforming the vector-insert into a suitable host;

(c) culturing transformed host under conditions allowing for replication of the vector-insert;

(d) recovering the vector-insert from said host; and

(e) digesting the vector-insert with one or more restriction enzymes, thereby releasing said insert; and

(f) comparing the size of the insert to sizes of fragments generated by the same restriction enzyme or enzymes in said reference nucleic acid or nucleic acids.

18. The method of claim 1, wherein comparing is by determining at least a portion of the nucleotide sequence of the first nucleic acid sequence and comparing the nucleotide sequence to the nucleotide sequence of one or more reference nucleic acids.

19. The method of claim 1, wherein comparing is by hybridizing the first nucleic acid sequence to one or more of the reference nucleic acid sequences.

20. A method for equalizing the representation of nucleic acids in a population of nucleic acids, the method comprising:

(a) providing a population of nucleic acid sequences, wherein said population comprises a first nucleic acid and a second nucleic acid having a nucleic acid sequence distinct from the first nucleic acid, and wherein said first nucleic acid is present at a higher level in said population than said second population;

(b) partitioning said population into one or more subpopulations of nucleic acids; and

(c) comparing the levels of said first nucleic acid sequence to the levels of said second nucleic acid sequence in the subpopulation of nucleic acid sequences, wherein a lower

level of the first nucleic acid sequence relative to the second nucleic acid sequence indicates the representation of said first and second nucleic acid sequences are normalized.

21. A method for producing a population of nucleic acid molecules enriched for 5' regions of mRNA molecules, the method comprising:

(a) providing a population of RNA molecules, said population including RNA molecules having a 5' terminal Gppp cap structure and a 5' terminal phosphate group;

(b) contacting said population of RNA molecules with a phosphatase under conditions that result in removal of the 5' terminal phosphate group while leaving the 5' terminal Gppp cap structure intact;

(c) inactivating said phosphatase;

(d) contacting the population of RNA molecules with a pyrophosphatase under conditions that result in the removal of the 5' terminal Gppp and the formation of a 5' phosphate group;

(e) annealing an oligonucleotide in the presence of an RNA ligase to form a hybrid molecule; and

(f) forming a cDNA from said oligonucleotide.

22. A method of identifying an RNA sequence in a sample comprising a plurality of RNA sequences, the method comprising:

(a) synthesizing cDNA copies of a plurality of RNA species to form a cDNA sample;

(b) determining the size of one or more of said cDNA molecules in said cDNA sample;

(c) comparing the size of said sample with the size of a reference nucleic acid; and

(d) thereby identifying the cDNA sequence.

23. The method of claim 22, wherein said cDNA molecules are digested with one or more restriction enzymes prior to the determining step.

24. The method of claim 23, further comprising ligating adapter oligonucleotides to the termini of the digested cDNA molecules prior to the determining step.

25. The method of claim 22, wherein said identifying step comprises comparing the size of one or more digestion products produced by one or more said cDNA molecules to a reference nucleic acid or nucleic acids.

26. A method of identifying an RNA sequence in a population of RNA sequences, the method comprising:

(a) removing 5' terminal pppG from RNAs in said population to form a population of RNAs having terminal 5' phosphate groups;

(b) ligating a linker oligonucleotide to the terminal 5' phosphate groups of RNA molecules in said population of RNAs;

(c) synthesizing complementary cDNA molecules from said population of RNA molecules to form a cDNA sample;

(d) digesting said complementary cDNA molecules with at least one restriction enzyme;

(e) ligating an adapter molecule to the digested cDNA molecules;

(f) amplifying the molecules produced in step (e);

(g) identifying the amplified molecules of step (f); and

(h) comparing the amplified molecules to one or more reference nucleic acids.

27. A method of identifying a nucleic acid sequence, the method comprising:

(a) providing a population of nucleic acid molecules comprising at least a first subset of nucleic acid molecules, the first subset of nucleic acid molecule further comprising at least a second subset of nucleic acid molecules;

(b) separating the first subset of nucleic acid molecules from other nucleic acid molecules in the population of nucleic acid molecules;

(c) isolating the first subset of nucleic acid molecules;

(d) constructing a library with the isolated first subset of nucleic acid molecules, wherein one or more members of the library comprises the second subset of nucleic acid molecules and wherein one or more members of the library is distinguishable from at least one of the other members of the library;

(e) recovering nucleic acids from one or more members of the library;

(f) separating the second subset of nucleic acid molecules from at least some of the other members in the library;

(g) isolating at least one nucleic acid molecule from the second subset of nucleic acid molecules; and

(h) sequencing the nucleic acid molecule, thereby identifying a nucleic acid sequence.

28. The method of claim 27, wherein the population of nucleic acid molecules is amplified using a first primer and a second primer.

29. The method of claim 27, wherein the population of nucleic acid molecules is provided as a pluraltity of cDNA molecules.

30. The method of claim 29, wherein the cDNA molecules comprise a library selected from the group consisting of a collection of sequences derived from the 5' end of RNA molecules, a library derived from the internal regions of RNA molecules, and a library derived from the 3' end of RNA molecules.

31. The method of claim 30, wherein the library is amplified using a first primer and a second primer.

32. The method of claim 27, wherein the population of nucleic acids comprises genomic DNA.

33. The method of claim 27, wherein the population of nucleic acids comprises a normalized population of nucleic acids.

34. The method of claim 27, wherein the first subset of nucleic acid molecules are separated from other nucleic acids in the population of nucleic acids by size.

35. The method of claim 34, wherein said separation is by electrophoresis.

36. The method of claim 35, wherein the electrophoresis is polyacrylamide gel electrophoresis.

37. The method of claim 35, wherein the electrophoresis is agarose gel electrophoresis.

38. The method of claim 27, wherein the members of the first subset of nucleic acids differ by 20 or fewer nucleotides in length.

39. The method of claim 27, wherein the members of the first subset of nucleic acids differ by 15 or fewer nucleotides in length.

40. The method of claim 27, wherein the members of the first subset of nucleic acids differ by 12 or fewer nucleotides in length.

41. The method of claim 27, wherein the members of the first subset of nucleic acids differ by 8 or fewer nucleotides in length.

42. The method of claim 27, wherein the members of the first subset of nucleic acids differ by 6 or fewer nucleotides in length.

43. The method of claim 27, wherein the population of nucleic acids comprises nucleic acids

having terminal sequences identical to those produced by digestion of a nucleic acid molecule with one or more restriction endonucleases.

44. The method of claim 43, wherein the restriction endonuclease is a Type II or Type IIS restriction endonuclase.

45. The method of claim 43, wherein the restriction endonuclease recognizes a four nucleotide recognition sequence.

46. The method of claim 43, wherein the restriction endonuclease recognizes a six nucleotide recognition sequence.

47. The method of claim 27, wherein the library is prepared by a process comprising:

(a) ligating the isolated first subset of nucleic acid molecules to a vector to form a population of vector-insert nucleic acid molecules;

(b) transforming the vector-insert nucleic acid molecules into a host cell to form a library; and

(c) culturing the library under conditions that allow for at least some members of the library to be distinguished from other members of the library.

48. The method of claim 27, wherein one or more members of the library is spatially distinguishable from other members of the library.

49. The method of claim 47, wherein one or more members of the library is spatially distinguishable from other members of the library.

50. The method of claim 27, wherein two or more members of the library are combined prior to separating the second subset of nucleic acid molecules.

51. The method of claim 27, wherein the second subset of nucleic acid molecules are

separated by size.

52. The method of claim 27, wherein the second subset of nucleic acid molecules are separated by electropheresis.

53. The method of claim 52, wherein said electrophoresis is in a replaceable matrix formulation comprising

(a) a linear polyacrylamide (LPA) solution, wherein the LPA concentration in said solution ranges between 1% to 3% (w/w);

(b) at least one denaturant;

(c) a buffer; and

(d) 3 M to 8 M urea, wherein the formulation is capable of separating nucleic acids.

54. The method of claim 27, wherein the nucleic acid molecule is compared to one or more known nucleic acid sequences prior to sequencing.

55. The method of claim 27, wherein the nucleic acids recovered from one or more members of the library are pooled prior to sequencing.